

Gencore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:34 ; Search time 17.21 Seconds

(without alignments)  
103.206 Million cell updates/sec

Title: US-09-331-631A-25\_COPY\_31\_85

Perfect score: 315

Sequence: 1 ENPKHNCLOSCNSERDSYR.....EEEEGEI<sup>P</sup>PRPRPRPQHPER 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

RESULT	1	GLCA_SOYBN	STANDARD;	PRT;	605 AA.
ID	GLCA_SOYBN				
AC	P13916;				
DT	01-JAN-1990	(Rel. 13, Created)			
DT	01-APR-1990	(Rel. 14, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	BETA-CONGLYCANIN, ALPHA CHAIN PRECURSOR.				
OS	Glycine max (Soybean).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-COTYLEDON;				
RX	Medline:9135860; PubMed=2103438;				
RA	Sebastiani F.L., Farrel L.B., Schuler M.A., Beachy R.N.:				
RT	"Complete sequence of a cDNA of alpha subunit of soybean beta-conglycanin";				
RT	Plant Mol. Biol. 15:197-201(1990).				
CC	-I- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE A CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.				
CC	-I- SUBUNIT: THE ALPHA', ALPHA', AND BETA SUBUNITS ASSOCIATE IN VARIOUS COMBINATIONS.				
CC	-I- SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN BODIES, TO FORM TRIMERIC PROTEINS.				
CC	-I- SIMILARITY: TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VICTILIN, CONVICILIN, CONGLYCANIN, ETC.).				
CC	-----				
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CC	-----				
DR	EMBL; X17698; CAA35691.1; -				
DR	PIR; S14681; FWIBA.				
DR	ISSP; P50477; ICRAW.				
DR	INTERPRO; IPR001113; -				
DR	INTERPRO; IPR001113; -				
PFAM; PF00546; Seedstore_7s; 1.					
DR	SEED; Storage_protein; Signal; Glycoprotein; Multigene family.				
KW	Seed storage protein; Signal; Glycoprotein; Multigene family.				
FT	SIGNAL	1	22		
FT	PROPEP	23	62		
FT	CHAIN	63	605	BETA-CONGLYCANIN, ALPHA CHAIN.	
FT	CARBONID	261	261	N-LINKED (GUCNAC. . .) (POTENTIAL).	
FT	CARBONID	517	517	N LINKED (GUCNAC. . .) (POTENTIAL).	
SEQUENCE	605 AA:	70293 MW:	CBEBA30506BBBC57 CRC64;		
Query Match	100.0%	Score 315; DB 1; Length 605;			
Best local Similarity	100.0%	Pred. No. 1.6e-26;			
Matches	55;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY 1 ENPKHNCLOCSNSERDSYRQACHARCNLKVKEECEGEIPRPRPQPER 55  
 Db 31 ENPKHNCLOCSNSERDSYRQACHARCNLKVKEECEGEIPRPRPQPER 85

RESULT 2

ID GLCX SOYBN STANDARD; PRT; 639 AA.

ID GLCX SOYBN STANDARD; PRT; 639 AA.

AC P11827; (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DR 01-AUG-1992 (Rel. 23, Last annotation update)

DE BETA-CONGLYCINTIN, ALPHA' CHAIN PRECURSOR.

GN CG-1.

OS Glycine max (Soybean).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Fabales; Fabaceae; Papilionoideae; Glycine.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86250867; PubMed=3013879;

RA Doyle J.J., Schuler M.A., Godet W.D., Zenger V., Beachy R.N.,

RT Sligothorn J.L.; Schuler M.A.,

RT "The glycosylated seed storage proteins of Glycine max and Phaseolus vulgaris. Structural homologies of genes and proteins.",

RT R.L. Biol. Chem. 261:9228-9238(1986).

RN [2]

RP SEQUENCE OF 340-639 FROM N.A.

RX MEDLINE=831343289; PubMed=6897678;

RA Schuler M.A., Ladin B.F., Pollaco J.C., Freyer G., Beachy R.N.;

RT "Structural sequences are conserved in the genes coding for the alpha, alpha', and beta-subunits of the soybean 7S seed storage protein.",

RT R.L. Nucleic Acids Res. 10:8245-8261(1982).

CC -!- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE A CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.

CC -!- SUBUNIT: THE ALPHA', ALPHA, AND BETA-SUBUNITS ASSOCIATE IN VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.

CC -!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.

CC -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCINTIN, ETC.).

RN [3]

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CC DR EMBL: L38953; AAA60336.1; -.

CC DR HSSP: 150477; ICAN.

CC DR INTERPRO: IPR001113; -.

CC DR PFAM: PF00546; Seedstore\_7s; 1.

CC DR KW Allergen.

CC SQ SEQUENCE 614 AA; 70283 MW; IDAAC21/EECSF31 CRC64;

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CC DR EMBL: P02653; 2PHL.

CC DR INTERPRO: IPR001113; -.

CC DR PFAM: PF00546; Seedstore\_7s; 2.

CC KW Seed storage protein; Signal; Glycoprotein; Multi gene family.

FT SIGNAL 1

FT PROPER 23 62

FT CHAIN 63 639 BETA-CONGLYCINTIN, ALPHA' CHAIN

FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 551 551 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 543 543 P -> L (IN REF. 2).

FT CONFLICT 549 549 M -> V (IN REF. 2).

FT CONFLICT 608 608 S -> T (IN REF. 2).

FT SEQUENCE 639 AA; 74325 MW; 469BF24C79651E3F CRC64;

QY 1 ENPKHNCLOCSNSERDSYRQACHARCNLKVKEECEGEIPRPRPQPER 55  
 Db 31 ENPKHNCLOCSNSERDSYRQACHARCNLKVKEECEGEIPRPRPQPER 84

RESULT 3

ID AH12\_ARAHY STANDARD; PRT; 614 AA.

ID AH12\_ARAHY STANDARD; PRT; 614 AA.

AC P43237; (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE ALLERGEN ARA H 1, CLONE P41B (ARA H 1).

OS Arachis hypogaea (Peanut).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Fabales; Fabaceae; Papilionoideae; Arachis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. FLORUNNER;

RX MEDLINE=96013631; PubMed=756062;

RA Burks A.W., Cockrell G., Stanley J.S., Helm R.M., Bannon G.A.;

RT "Recombinant peanut allergen Ara h 1 expression and IgE binding in patients with peanut hypersensitivity.",

Query Match 82.4%; Score 259.5; DB 1; Length 639;  
 Best Local Similarity 83.9%; Pred. No. 1.3e-20; Matches 47; Conservative 5; Mismatches 1; Indels 3; Gaps 2;

RL J. Clin. Invest. 96:1715-1721(1995).  
 CC -!- SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,  
 CONVICILIN, CONGLYCININ, ETC.).  
 CC -----  
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 CC -----  
 DR EMBL; L24402; AAB00861.1; -.  
 DR HSSP; P50477; 1CAX.  
 DR INTERPRO; IPR00113; -.  
 DR PFAM; PF00546; Seedstore\_7s; 1.  
 KW Allergen.  
 CC SEQUENCE 626 AA; 71345 MW; 1A6BBBE41490D0E3 CRC64;  
 SQ -----  
 RESULT 5  
 TONE\_PASHA  
 ID TONE\_PASHA STANDARD: PRT; 246 AA.  
 AC P72204;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE TONB PROTEIN.  
 GN OS Pasteurellaceae; gamma subdivision; Pasteurellaceae;  
 OC Bacteria; Proteobacteria; Pasteurellales;  
 OC Pasteurellales.  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN-SEROTYPE A1 / ATCC 43270;  
 RA Graham M.R., Lo R.Y.C.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -----  
 CC -!- FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT  
 CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO  
 THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO  
 TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-  
 REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE  
 RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER  
 CC MEMBRANE PROTEINS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ANCHORED TO THE CYTOPLASMIC  
 CC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE  
 CC PERIPLASM (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE TONB FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M16891; AAM33071.1; -.  
 DR HSSP; P50477; 1CAX.  
 DR INTERPRO; IPR00113; -.  
 DR PFAM; PF00546; Seedstore\_7s; 1.  
 KW Seed storage protein; Signal  
 FT SIGNAL 1 25  
 CHAIN 26 588 AA; VICILIN C72.  
 SQ SEQUENCE 588 AA; 63E693B29AB8ADEB CRC64;  
 RESULT 6  
 VCUB\_GOSHI  
 ID VCUB\_GOSHI STANDARD: PRT; 588 AA.  
 AC P09801;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).  
 OS Gossypium hirsutum (Upland cotton).  
 OC Euphorbiidae; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II;  
 OC Malvales; Malvaceae; Gossypium.  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA Chian C.A., Pyle J.B., Legocki A.B., Dure L. III;  
 RL Plant Mol. Biol. 7:475-489(1986).  
 CC -!- FUNCTION: SEED STORAGE PROTEIN.  
 CC -!- SUBCELLULAR LOCATION: COLEOPTILAR VACUOLAR PROTEIN  
 CC BODIES.  
 CC -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,  
 CONVICILIN, CONGLYCININ, ETC.).  
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 CC -----  
 DR EMBL; M16891; AAM33071.1; -.  
 DR PIR; A10838; FWCNAB.  
 DR HSSP; P50477; 1CAX.  
 DR INTERPRO; IPR00113; -.  
 DR PFAM; PF00546; Seedstore\_7s; 1.  
 KW Seed storage protein; Signal  
 FT SIGNAL 1 25  
 CHAIN 26 588 AA; VICILIN C72.  
 SQ SEQUENCE 588 AA; 63E693B29AB8ADEB CRC64;  
 RESULT 7  
 YN3\_CABEL  
 ID YN3\_CABEL STANDARD: PRT; 3051 AA.  
 AC P34576;  
 DT 01-FEB-1994 (Rel. 28, Created)



FT	DISULFID	1105	1122	BY SIMILARITY.	RN	[1]
FT	DISULFID	1124	1143	BY SIMILARITY.	RP	SEQUENCE FROM N.A.
FT	DISULFID	1150	1164	BY SIMILARITY.	RX	Medline:95054311; Published=7/4/324;
FT	DISULFID	1157	1173	BY SIMILARITY.	RA	Jonk, L.J.C., de Jonge, M.J., Pals, C.E.G.M., Wissink, S.,
FT	DISULFID	1175	1194	BY SIMILARITY.	RA	Verhaar, J.M.A., Schoorlemmer, J., Kruijter, W.,
FT	DISULFID	1201	1214	BY SIMILARITY.	RT	"Cloning and expression during development of three murine members of the Coup family of nuclear orphan receptors."
FT	DISULFID	1208	1223	BY SIMILARITY.	RT	Mech. Dev. 47:81-97(1994).
FT	DISULFID	1225	1244	BY SIMILARITY.	RL	[2]
FT	DISULFID	1251	1264	BY SIMILARITY.	RL	SEQUENCE FROM N.A.
FT	DISULFID	1258	1273	BY SIMILARITY.	RP	TISSUE=PIUTUTARY;
FT	DISULFID	1275	1294	BY SIMILARITY.	RC	Medline:9422589; Pubmed=8194772;
FT	DISULFID	1302	1315	BY SIMILARITY.	RX	Barnhart, K.M., Mellon, P.L.;
FT	DISULFID	1309	1324	BY SIMILARITY.	RA	"The sequence of a murine cDNA encoding Ear-2, a nuclear orphan receptor."
FT	DISULFID	1326	1345	BY SIMILARITY.	RT	Gene 142:313-314(1994)
FT	DISULFID	1356	1372	BY SIMILARITY.	RL	-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
FT	DISULFID	1364	1381	BY SIMILARITY.	CC	-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
FT	DISULFID	1383	1395	BY SIMILARITY.	CC	NR2 SUBFAMILY.
FT	DISULFID	1401	1415	BY SIMILARITY.	CC	-----
FT	DISULFID	1409	1424	BY SIMILARITY.	CC	-----
FT	DISULFID	1426	1443	BY SIMILARITY.	CC	-----
FT	DISULFID	1450	1464	BY SIMILARITY.	CC	-----
FT	DISULFID	1458	1473	BY SIMILARITY.	CC	-----
FT	DISULFID	1475	1491	BY SIMILARITY.	CC	-----
FT	DISULFID	1498	1512	BY SIMILARITY.	CC	-----
FT	DISULFID	1506	1521	BY SIMILARITY.	CC	-----
FT	DISULFID	1523	1541	BY SIMILARITY.	CC	-----
FT	DISULFID	1548	1562	BY SIMILARITY.	CC	-----
FT	DISULFID	1556	1571	BY SIMILARITY.	CC	-----
FT	DISULFID	1573	1591	BY SIMILARITY.	CC	-----
FT	DISULFID	1598	1611	BY SIMILARITY.	CC	-----
FT	DISULFID	1605	1620	BY SIMILARITY.	DR	DR EMBL; L25674; AA37532; 1; -.
FT	DISULFID	1622	1641	BY SIMILARITY.	DR	DR HSSP; P19793; 2NLL.
FT	DISULFID	1648	1661	BY SIMILARITY.	DR	DR MGD; MGI:99530; ERBAL2.
FT	DISULFID	1655	1670	BY SIMILARITY.	DR	DR INTERPRO; IPR00536; -.
FT	DISULFID	1672	1691	BY SIMILARITY.	DR	DR INTERPRO; IPR001628; -.
FT	DISULFID	1697	1709	BY SIMILARITY.	DR	DR INTERPRO; IPR001723; -.
FT	DISULFID	1703	1719	BY SIMILARITY.	DR	DR INTERPRO; IPR003068; -.
FT	DISULFID	1721	1738	BY SIMILARITY.	DR	DR PFAM; PF00104; hormone_rec; 1.
FT	DISULFID	1744	1758	BY SIMILARITY.	DR	DR PFAM; PF00105; zf-C4; 1.
FT	DISULFID	1752	1767	BY SIMILARITY.	DR	DR PRINTS; PR00398; STR01DFINGER.
FT	DISULFID	1769	1787	BY SIMILARITY.	DR	DR PRINTS; PR01282; COUPINFACT0R.
FT	DISULFID	1801	1815	BY SIMILARITY.	DR	DR PROSITE; PS00031; NUCLEAR RECEPTOR.
FT	DISULFID	1825	1829	BY SIMILARITY.	KW	Receptor; transcription regulation; DNA-binding; nuclear protein;
FT	DISULFID	1827	1845	BY SIMILARITY.	KW	Zinc finger.
FT	DISULFID	1853	1867	BY SIMILARITY.	FT	DNA_BIND 57 122 C4-TYPE ZINC FINGERS (TWO).
FT	DISULFID	1861	1878	BY SIMILARITY.	FT	ZN_FING 57 77 C4-TYPE.
FT	DISULFID	1880	1899	BY SIMILARITY.	FT	ZN_FING 93 117 C4-TYPE.
FT	DISULFID	1906	1920	BY SIMILARITY.	FT	CONFFLICT 10 10 D -> G (IN REF. 2).
FT	DISULFID	1914	1929	BY SIMILARITY.	FT	CONFFLICT 152 152 P -> H (IN REF. 2).
FT	DISULFID	1931	1949	BY SIMILARITY.	FT	CONFFLICT 164 165 QL -> HV (IN REF. 2).
FT	DISULFID	1956	1970	BY SIMILARITY.	FT	CONFFLICT 196 198 LIF -> AV (IN REF. 2).
FT					FT	CONFFLICT 239 241 LPL -> VAV (IN REF. 2).
FT					FT	CONFFLICT 357 357 K -> Q (IN REF. 2).
FT					SQ	SEQUENCE 390 AA: 41982 MW: 4C27F4390AF15PF CRC64;
RESULT	8					
Query	2	NPKHNKQQS-CNSERDSYRQACHARCNLKEKECEEGEI---PRPRPRPQHP 53				
TD	EAR2_MOUSE	STANDARD;	PRT;	390 AA.		
AC	PA3136; Q61504;					
DT	01-NOV-1995 (Rel. 32, Created)					
DT	01-NOV-1995 (Rel. 32, Last sequence update)					
DE	ORPHAN NUCLEAR RECEPTOR EAR-2 (V-ERBA RELATED PROTEIN EAR-2).					
GN	NR2F6 OR ERBA2 OR EAR2 OR EAR-2.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathli; Muridae; Murinae; Mus.					
RESULT	9					
Query	11	SNSERD---SYRQACHAR---CNLKEKECEEGEI-PRRPRP 50				
TD	EAR2_RAT	STANDARD;	PRT;	390 AA.		
ID	EAR2_RAT					
AC	Q00901;					
DT	30-MAY-2000 (Rel. 39, Created)					
DT	30-MAY-2000 (Rel. 39, Last sequence update)					
DT	01-OCT-2000 (Rel. 40, Last annotation update)					
DE	ORPHAN NUCLEAR RECEPTOR EAR-2 (V-ERBA RELATED PROTEIN EAR-2)					



CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS: MULTIPLE ISOFORMS ARE CREATED BY ALTERNATIVE  
 CC SPLICING EVENTS, WHICH SEEM TO OCCUR IN A TISSUE-SPECIFIC MANNER.  
 CC THE SEQUENCE SHOWN HERE IS THAT OF CACM4A. THE REGION SEQUENCED IN  
 CC ROB3 AND RKC5 IS IDENTICAL TO CACM4.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PANCREATIC ISLETS AND B-  
 CC LYMPHOCTYES.  
 CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC  
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 CC  
 CC  
 DR EMBL: D38101; BAA07282.1; -.  
 DR EMBL: D38102; BAA07283.1; -.  
 DR EMBL: M57682; AA42015.1; -.  
 DR EMBL: U44005; AA860515.1; -.  
 DR EMBL: M92221; AA840895.1; -.  
 DR EMBL: U3177; AA89156.1; -.  
 DR EMBL: U49126; AA81634.1; -.  
 DR EMBL: U49127; AA81635.1; -.  
 DR EMBL: U49128; AA81636.1; -.  
 DR EMBL: U49129; AA81637.1; -.  
 DR EMBL: U49130; AA81638.1; -.  
 DR EMBL: U49131; AA81639.1; -.  
 DR EMBL: U49132; AA81640.1; -.  
 DR EMBL: U49133; AA81641.1; -.  
 DR EMBL: U49134; AA81642.1; -.  
 DR EMBL: U49135; AA81643.1; -.  
 DR EMBL: U49136; AA81644.1; -.  
 DR EMBL: U49137; AA81645.1; -.  
 DR EMBL: U49138; AA81646.1; -.  
 DR EMBL: U49139; AA81647.1; -.  
 DR EMBL: U49140; AA81648.1; -.  
 DR EMBL: U49141; AA81649.1; -.  
 DR EMBL: U49142; AA81650.1; -.  
 DR EMBL: U49143; AA81651.1; -.  
 DR EMBL: U49144; AA81652.1; -.  
 DR EMBL: U49145; AA81653.1; -.  
 DR EMBL: U49146; AA81654.1; -.  
 DR EMBL: U49147; AA81655.1; -.  
 DR EMBL: U49148; AA81656.1; -.  
 DR EMBL: U49149; AA81657.1; -.  
 DR EMBL: U49150; AA81658.1; -.  
 DR EMBL: U49151; AA81659.1; -.  
 DR EMBL: U49152; AA81660.1; -.  
 DR EMBL: U49153; AA81661.1; -.  
 DR EMBL: U49154; AA81662.1; -.  
 DR EMBL: U49155; AA81663.1; -.  
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CC EMBL: M31641; AAA02688.1; -.  
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 DR KW SIGNAL; Antigen; Glycoprotein; Transmembrane; Repeat.  
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 FT TRANSMEM 680 708 EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
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 FT CARBOHYD 289. N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT VARIANT 582 582 A -> T (IN STRAIN ADELAIDE-1).  
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Query Match 18.7%; Score 59; DB 1; Length 713;  
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 GN MST101(2);  
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 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
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 RX MEDLINE=94200512; PubMed=8150205;  
 RA Neesen J., Bumemann H., Heinlein U.A.;  
 RT "The Drosophila hydei gene Dhmt101(1) encodes a testis-specific, repetitive, axoneme-associated protein with differential abundance in Y chromosomal deletion mutant flies.";  
 RL Dev. Biol. 162:414-25(1994).  
 CC -!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.  
 CC -!- TISSUE SPECIFICITY: TESTIS.  
 CC -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.

RESULT 14  
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 RA Neesen J., Bumemann H., Heinlein U.A.;  
 RT "The Drosophila hydei gene Dhmt101(1) encodes a testis-specific, repetitive, axoneme-associated protein with differential abundance in Y chromosomal deletion mutant flies.";  
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 CC -!- TISSUE SPECIFICITY: TESTIS.  
 CC -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.

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CC EMBL: X73481; CAAS1876.1; -.  
 CC PIR: S34154; S34154.  
 DR HISP: P01032; ICPA.  
 DR FLIBASE; FBgn001816; Dhyd1mst101.

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 Matches 12; Conservative 9; Mismatches 19; Indels 2; Gaps 1;

QY 1 ENPKHKNKQLOQSCNSERDYSRNRQACHARNLK--VEREECERGE 40  
 AC Q07408;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE OCTOPAMINE RECEPTOR 1 (OAL).  
 DE Lymanea stagnalis (Great pond snail).  
 DE Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Lymnaea.  
 RN [1]  
 RR SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=CNS;  
 RX MEDLINE=97347296; PubMed=9203635;  
 RA Gerhardt C.C., Balkier R.A., Piek G.J., Planta R.J., Vreugdenhil E., Leyser J.E., van Heerikhuizen H.;  
 RT "molecular cloning and pharmacological characterization of a molluscan octopamine receptor;"  
 RT Mol. Pharmacol. 51:293-300(1997).  
 RL -!- FUNCTION: G-PROTEIN COUPLED RECEPTOR FOR OCTOPAMINE (OA), WHICH IS A NEUROTRANSMITTER, NEUROHORMONE, AND NEUROMODULATOR IN INVERTEBRATES. ACTIVATION OF THIS RECEPTOR BY OCTOPAMINE INDUCES AN INCREASE IN BOTH INOSITOL PHOSPHATES AND CYCLIC AMP. THE COUPLING TO ADENYLYL CYCLASE SEEMS TO BE LESS EFFICIENT THAN THE COUPLING TO PHOSPHOLIPASE C. THE RANK ORDER OF POTENCY FOR AGONISTS IS P-SYNEPHRINE > CLONIDINE > P-OCTOPAMINE = XLOMETHAZOLINE = PHENYLEPHRINE = OXYMETAZOLINE > B-HT920 > SEROTONIN = P-TYRAMINE > EPINEPHRINE > NOREPINEPHRINE > METHOXAMINE = DOPAMINE = HISTAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE > CHIOPROMAZINE / SPIPERONE > PHEWOLAMINE > MANSERINE > RAUWOLSCINE > PRAZOSIN > ALPRENOLOL / PROPARANOLOL > PINOOL.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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or send an email to [bioinf@infobiogen.fr](mailto:bioinf@infobiogen.fr)

DR	PRINTS: PRO0237; GPCRHHODPSN.
DR	PROSITE: PS00237; G-PROTEIN_RECPR_FL_1; 1.
DR	PS05262; G-PROTEIN_RECPR_FL_2; 1.
KW	G-protein coupled receptor; Transmembrane; glycoprotein.
FT	DOMAIN 1 28
FT	TRANSMEM 29 53
FT	DOMAIN 54 64
FT	TRANSMEM 65 87
FT	DOMAIN 88 102
FT	TRANSMEM 103 124
FT	DOMAIN 125 147
FT	TRANSMEM 148 167
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Matches	16;	Conservative	8;	Mismatches
			17;	Indices
			13;	Gaps
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Search completed: March 1, 2001, 16:20:36  
Job time: 211 sec

Search completed!